+T,0730

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Franz-Bacon, Karin
Gorman, Daniel M.
McClanahan, Terrill K.

(ii) TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US not yet assigned
(B) FILING DATE: 18-JUN-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/050,156
(B) FILING DATE: 17-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0744K

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-852-9196
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

aa

(A) NAME/KEY: CDS
(B) LOCATION: 47..370

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 101..370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GTGTGCCGGA TTTGGTTAGC TGAGCCCACC GAGAGGCGCC TGCAGG ATG AAA GCT          55
                                                   Met Lys Ala
                                                   -18

CTC TGT CTC CTC CTC CTC CCT GTC CTG GGG CTG TTG GTG TCT AGC AAG         103
Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val Ser Ser Lys
-15                 -10                 -5                  1

ACC CTG TGC TCC ATG GAA GAA GCC ATC AAT GAG AGG ATC CAG GAG GTC         151
Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile Gln Glu Val
              5                  10                  15

GCC GGC TCC CTA ATA TTT AGG GCA ATA AGC AGC ATT GGC CTG GAG TGC         199
Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly Leu Glu Cys
         20                  25                  30

CAG AGC GTC ACC TCC AGG GGG GAC CTG GCT ACT TGC CCC CGA GGC TTC         247
Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro Arg Gly Phe
     35                  40                  45

GCC GTC ACC GGC TGC ACT TGT GGC TCC GCC TGT GGC TCG TGG GAT GTG         295
Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser Trp Asp Val
 50                  55                  60                  65

CGC GCC GAG ACC ACA TGT CAC TGC CAG TGC GCG GGC ATG GAC TGG ACC         343
Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met Asp Trp Thr
                 70                  75                  80

GGA GCG CGC TGC TGT CGT GTG CAG CCC TGAGGTCGCG CGCAGCGCGT               390
Gly Ala Arg Cys Cys Arg Val Gln Pro
             85                  90

GCACAGCGCG GGCGGAGGCG GCTCCAGGTC CGGAGGGGTT GCGGGGGAGC TGGAAATAAA      450

CCT                                                                    453
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Lys Ala Leu Cys Leu Leu Leu Pro Val Leu Gly Leu Leu Val
-18         -15                 -10                  -5

Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
          1               5                  10

Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
 15                  20                  25                  30

Leu Glu Cys Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
                35                  40                  45

Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
             50                  55                  60

Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
         65                  70                  75

Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
     80                  85                  90
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTGGCTHYG SCTGTGGMTC KTGG 24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCAGCGSG CWSHKGTCCA GTC 23